

BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (936 letters)

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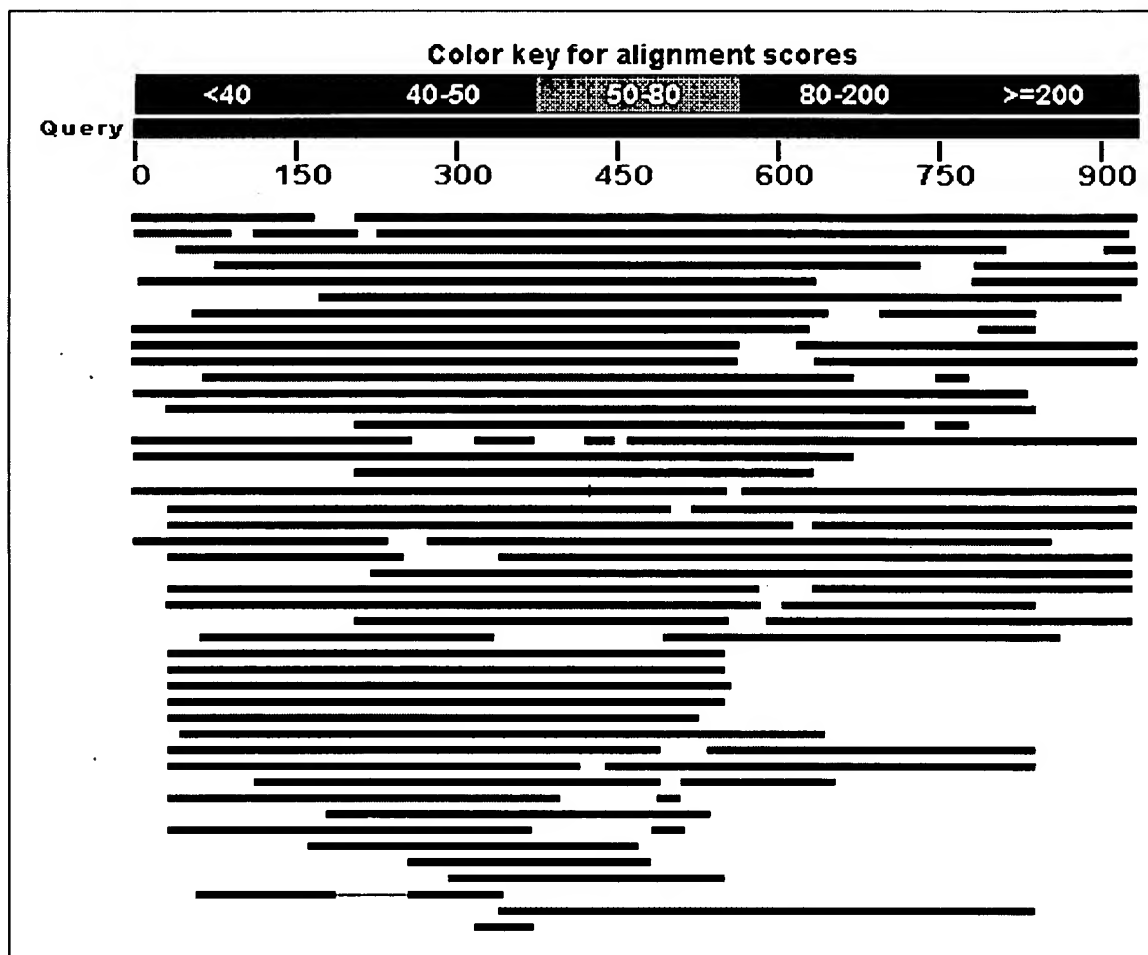
New Search

BLASTN 2.2.16 (Mar-25-2007)

RID: 6KAUYH52014 Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions
43,364,352 sequences; 23,803,995,170 total letters

Query= Length=936

Distribution of 76 Blast Hits on the Query Sequence



Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map View

Sequences producing significant alignments:

(Click headers to sort columns)

BI457762.1	603198412F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5277746 5', mRNA sequence	1312	1312	77%	0.0	99%	U
BI913953.1	603183395F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5247551 5', mRNA sequence	1284	1284	74%	0.0	99%	U
AV703309.1	AV703309 ADB Homo sapiens cDNA clone ADBBFB03 5', mRNA sequence	1218	1218	82%	0.0	95%	U
AV701492.1	AV701492 ADB Homo sapiens cDNA clone ADBANH10 5', mRNA sequence	1208	1208	70%	0.0	99%	U
EL733651.1	9311 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC037246, mRNA sequence	1166	1166	67%	0.0	99%	U
EB523840.1	297886 Pigtailed macaque ovary library Macaca nemestrina cDNA 3', mRNA sequence	1151	1151	79%	0.0	94%	
BM710229.1	UI-E-CI1-age-b-20-0-UI.r1 UI-E-CI1 Homo sapiens cDNA clone UI-E-CI1-age-b-20-0-UI 5', mRNA sequence	1088	1088	63%	0.0	99%	U
BI819400.1	603034575F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175571 5', mRNA sequence	1072	1072	67%	0.0	97%	U
BP197959.1	BP197959 Sugano cDNA library, adrenal gland Homo sapiens cDNA clone ADG07388 5', mRNA sequence	1050	1050	60%	0.0	100%	U
BP197915.1	BP197915 Sugano cDNA library, adrenal gland Homo sapiens cDNA clone ADG07288 5', mRNA sequence	1027	1027	60%	0.0	99%	U
AW951884.1	EST363954 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence	1022	1022	64%	0.0	96%	U
BX926574.2	BX926574 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0019.g.12 5prim, mRNA sequence	939	939	89%	0.0	87%	U
BX674168.2	BX674168 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0038.j.09 5prim, mRNA sequence	917	917	86%	0.0	87%	U
BG394800.1	602457137F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579665 5', mRNA sequence	902	902	54%	0.0	98%	U
AV703457.1	AV703457 ADB Homo sapiens cDNA clone ADBCWH10 5', mRNA sequence	876	876	50%	0.0	100%	U
BX667933.1	BX667933 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0026i.k.19 5prim, mRNA sequence	789	789	71%	0.0	87%	U
DB489677.1	DB489677 RIKEN full-length enriched human cDNA library, hypothalamus Homo sapiens cDNA clone H033028L10 5', mRNA sequence	784	784	45%	0.0	99%	U
AV705715.1	AV705715 ADB Homo sapiens cDNA clone ADBCYC06 5', mRNA sequence	771	907	59%	0.0	99%	U
BX280348.1	BX280348 NIH_MGC_96 Homo sapiens cDNA clone IMAGp998H0311701 ; IMAGE:5277746 5', mRNA sequence	758	758	44%	0.0	99%	U
EE973211.1	Q44820A FNM Bos taurus cDNA clone Q4482 5', mRNA sequence	699	699	62%	0.0	88%	U
BX667169.2	BX667169 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0026.k.19 3prim, mRNA sequence	675	675	62%	0.0	87%	U
EE973212.1	Q44821A FNM Bos taurus cDNA clone Q4482 3', mRNA sequence	673	673	62%	0.0	87%	U
AV725746.1	AV725746 HTC Homo sapiens cDNA clone HTCAHB10 5', mRNA sequence	673	673	39%	0.0	99%	U
CK775040.1	963851 MARC 2BOV Bos taurus cDNA 3', mRNA sequence	667	667	75%	0.0	83%	U

DY137128.1	000929BEMN030576HT BEMN Bos taurus cDNA, mRNA sequence	654	654	58%	0.0	88%	U
CX060692.1	PDUTs2048H03 Porcine testis cDNA library II Sus scrofa cDNA clone PDUTs2048H03 5' similar to homologue to ref NM_177505.2 Bos taurus phenylethanolamine N-methyltransferase (PNMT), mRNA, mRNA sequence	643	643	59%	0.0	87%	U
BE251193.1	601107280F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343723 5', mRNA sequence	643	643	37%	0.0	99%	U
AI880325.1	ap33a05.x1 Schiller astrocytoma Homo sapiens cDNA clone IMAGE:1957136 3' similar to gb:X52730_rna1 PHENYLETHANOLAMINE-N-METHYLTRANSFERASE (HUMAN);, mRNA sequence	636	636	39%	6e-179	97%	U
EM031252.1	496606 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	612	612	55%	9e-172	87%	U
BF076440.1	226007 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	610	610	55%	3e-171	87%	UE
BI976230.1	484991 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	608	608	56%	1e-170	87%	U
BE808641.1	213894 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	599	599	55%	7e-168	87%	U
BM664183.1	UI-E-CI1-age-b-20-0-UI.s1 UI-E-CI1 Homo sapiens cDNA clone UI-E-CI1-age-b-20-0-UI 3', mRNA sequence	584	584	33%	2e-163	100%	U
BE754888.1	208554 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	580	580	53%	3e-162	87%	U
BF775575.1	285767 MARC 3BOV Bos taurus cDNA 5', mRNA sequence	553	553	50%	6e-154	88%	U
BY721079.1	BY721079 RIKEN full-length enriched, adult male epididymis Mus musculus cDNA clone 9230023G19 5', mRNA sequence	545	545	64%	1e-151	83%	U
BE808590.1	213835 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	527	527	49%	3e-146	87%	U
N63192.1	yz85f05.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:289857 3' similar to gb:X52730_rna1 PHENYLETHANOLAMINE-N-METHYLTRANSFERASE (HUMAN);, mRNA sequence	475	475	32%	1e-130	95%	UE
CA392806.1	cs28h01.y2 Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs28h01 5', mRNA sequence	473	473	27%	5e-130	99%	U
T27687.1	EST12320 Human Uterus Homo sapiens cDNA 5' end similar to phenylethanolamine N-methyltransferase (HT:1278), mRNA sequence	444	444	29%	4e-121	95%	U
DY185707.1	000409BAGA004886HT BAGA Bos taurus cDNA, mRNA sequence	431	431	41%	3e-117	86%	U
DY080412.1	000407BAGA002500HT BAGA Bos taurus cDNA, mRNA sequence	424	424	40%	5e-115	86%	U
DY043824.1	000409BAGA005031HT BAGA Bos taurus cDNA, mRNA sequence	420	420	39%	6e-114	87%	U
BE106746.1	UI-R-B01-asr-f-11-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone UI-R-B01-asr-f-11-0-UI 3', mRNA sequence	416	416	42%	8e-113	85%	U
DY188095.1	000228BMPA999009HT BMPA Bos taurus cDNA, mRNA sequence	414	414	38%	3e-112	87%	U
DY077706.1	000315BAGA001737HT BAGA Bos taurus cDNA, mRNA sequence	392	392	36%	1e-105	87%	U
DY080460.1	000326BMPA002435HT BMPA Bos taurus cDNA, mRNA sequence	370	370	32%	6e-99	88%	U
BM658761.1	LZV602768483.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA sequence	329	329	36%	1e-86	84%	U
BE752632.1	205073 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	291	291	31%	5e-75	84%	U
BE752631.1	205072 MARC 2BOV Bos taurus cDNA 5', mRNA sequence	283	283	31%	8e-73	84%	U

DY083839.1	000330BMPA004088HT BMPA Bos taurus cDNA, mRNA sequence	276	276	24%	1e-70	88%	U
DR980845.1	SM016929 Placenta 3' EST Homo sapiens cDNA clone ID_16929 3', mRNA sequence	272	272	16%	2e-69	99%	U
DV902079.1	POSM0605021_B16R porcine skeletal muscle cDNA library (PoSM) Sus scrofa cDNA 3', mRNA sequence	259	259	27%	1e-65	85%	U
DY189365.1	000330BMPA004711HT BMPA Bos taurus cDNA, mRNA sequence	252	252	25%	2e-63	85%	U
BE110952.1	UI-R-BJ1-aux-g-12-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-aux-g-12-0-UI 3', mRNA sequence	239	239	25%	2e-59	85%	U
DY079272.1	000407BAGA003101HT BAGA Bos taurus cDNA, mRNA sequence	231	231	23%	3e-57	85%	U
CD556603.1	AGENCOURT_14477291 NIH_MGC_179 Homo sapiens cDNA clone IMAGE:30392582 5', mRNA sequence	222	222	18%	2e-54	90%	
DB559237.1	DB559237 RIKEN full-length enriched human cDNA library, hypothalamus Homo sapiens cDNA clone H033028L10 3', mRNA sequence	172	172	16%	2e-39	87%	
BF829680.1	MR2-HN0035-221200-019-a08 HN0035 Homo sapiens cDNA, mRNA sequence	165	165	10%	3e-37	96%	U
BU551882.1	mai22d03.y1 McCarrey Eddy type A spermatogonia Mus musculus cDNA clone IMAGE:6442901 5' similar to SW:PNMT_MOUSE P40935 PHENYLETHANOLAMINE N-METHYLTRANSFERASE ;, mRNA sequence	143	255	23%	1e-30	89%	U
BF408734.1	UI-R-BT1-bnf-e-09-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bnf-e-09-0-UI 3', mRNA sequence	139	139	15%	2e-29	83%	UE
DT397123.1	JGI_CABH11889.rev NIH_XGC_tropSkeMus1 Xenopus tropicalis cDNA clone IMAGE:7854648 3', mRNA sequence	89.8	89.8	53%	2e-14	71%	
DT397124.1	JGI_CABH11889.fwd NIH_XGC_tropSkeMus1 Xenopus tropicalis cDNA clone IMAGE:7854648 5', mRNA sequence	86.1	86.1	32%	3e-13	72%	
CN000669.1	ip02d06.b1 Brain - Cerebellum Library (DOGEST8) Canis familiaris cDNA clone ip02d06, mRNA sequence	75.0	75.0	5%	5e-10	90%	
DY082603.1	000313BMPA001406HT BMPA Bos taurus cDNA, mRNA sequence	73.1	73.1	9%	2e-09	81%	U
CX260010.1	1313390 NCCWA 02RT Oncorhynchus mykiss cDNA clone 02RT123G17 3', mRNA sequence	69.4	69.4	15%	3e-08	76%	
ES317490.1	AmisEST001436 Adult American Alligator Testis Library (Univ Florida Zoology) Alligator mississippiensis cDNA clone AMT5-4_G3_A07_1 similar to best hit in human is NNMT Nicotinamide N-methyltransferase; best hit in chicken is LOC776803 similar to Phenylethanolamine N-methyltransferase, mRNA sequence	47.3	47.3	5%	0.12	82%	
ES317140.1	AmisEST000973 Adult American Alligator Testis Library (Univ Florida Zoology) Alligator mississippiensis cDNA clone AMT5-4_G3_A07_1 similar to best hit in human is NNMT Nicotinamide N-methyltransferase; best hit in chicken is LOC776803 similar to Phenylethanolamine N-methyltransferase, mRNA sequence	47.3	47.3	5%	0.12	82%	
EG819500.1	EST_ssai_evd_21530 ssalevd thymus Salmo salar cDNA Salmo salar cDNA clone ssai_evd_527_311_fwd 5', mRNA sequence	41.7	41.7	2%	5.5	100%	U
CJ705520.1	CJ705520 Y.Ogihara unpublished cDNA library Wh_V4816 Triticum aestivum cDNA clone whv16n2e22 5', mRNA sequence	41.7	41.7	3%	5.5	90%	U
CJ600022.1	CJ600022 Y.Ogihara unpublished cDNA library Wh_V4816 Triticum aestivum cDNA clone rwhv16n2e22 3', mRNA sequence	41.7	41.7	3%	5.5	90%	U

DA184445.1	DA184445 BRAMY3 Homo sapiens cDNA clone BRAMY3002969 5', mRNA sequence	41.7	41.7	3%	5.5	90%	
CV359995.1	PM0-GN0498-210301-003-b09 GN0498 Homo sapiens cDNA, mRNA sequence	41.7	41.7	2%	5.5	93%	U
BM874128.1	laa01c10.x1 8 5 week embryo anterior tongue 8 5 EAT Homo sapiens cDNA 3' similar to TR:Q9Y6Y3 Q9Y6Y3 IDN3-B PROTEIN. ;, mRNA sequence	41.7	41.7	3%	5.5	90%	

Alignments

32

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Query	1	GGCAGCATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	57
AV703309	38	AG-CCCCTGACTCGGCC	53
EL733651	1	ATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	51
BI819400	218	GGCAGCATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	274
BP197959	15	GGCAGCATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	71
BP197915	15	GGCAGCATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	71
BX926574	11	GCAGCATGAGTGG-GACAGGCCAG-AGCCACGCTGCGGACGCGG-CCCCGACTCGGAC	66
BX674168	13	TGC-GGAGCTG-CCCCGACTCGGAC	36
BX667933	105	GCAGCATGAGTGG-GACAGGCCAG-AGCCACGCTGCGGACGCGG-CCCCGACTCGGAC	160
AV705715	8	GGCAGCATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	64
EE973211	13	GCGGGCGCGGTGCC- GACTCAGAC	36
DY137128	29	GCGGGCGCAGTGCCC- GACTCAGAC	52
CX060692	33	TGCGGACGCGG-CCCCGACTCGGAC	57
BM031252	9	GCGGGCGCGGTGCC- GACTCAGAC	32
BF076440	26	GCGGGCGCGGTGCC- GACTCAGAC	49
BI976230	24	GCGGGCGCGGTGCC- GACTCAGAC	47
BE808641	25	GCGGGCGCGGTGCC- GACTCAGAC	48
BE754888	9	GCGGGCGCAGTGCCC- GACTCAGAC	32
BF775575	7	GCGGGCGCGGTGCC- GACTCAGAC	30
BY721079	79	CCCTGACTCCGAC	91
BE808590	5	GCGGGCGCGGTGCC- GACTCAGAC	28
CA392806	313	GGCAGCATGAGCGGCG-CAGACC-GTAGCCCCAATGCGGGGCGCAG-CCCCTGACTCGGCC	369
DY185707	19	GCGGGCGCAGTGCCC- GACTCAGAC	42
DY043824	19	GCGGGCGCAGTGCCC- GACTCAGAC	42
DY077706	20	GCGGGCGCAGTGCCC- GACTCAGAC	43
DY189365	101	GCAGCATGAGCGG-GACAGACC-GGAGTCAGGCGGCGGCGCAGTGCCC- GACTCAGAC	156
DY079272	10	GCGGGCGCGGTGCC- GACTCAGAC	33
CD556603	355	GGCAGCATGAGCGGCG-CATACC-GTAGCCCCAATGCGGGGCGCAC-CCCCTGACTCGGCC	411
DY082603	106	GCAGCATGAGCGG-GACAGACC-GGAGTCAGGCGGCGGCGCAGTGCCC- GACTCAGAC	161

Query	58	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	116
AV703309	54	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	112
AV701492	1	CTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	40
EL733651	52	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	110
BM710229	1	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	59
BI819400	275	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	333
BP197959	72	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	130
BP197915	72	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	130
AW951884	1	GCGGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	51
BX926574	67	CCAGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	125
BX674168	37	CCAGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	95
BX667933	161	CCAGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	219
AV705715	65	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTCCG	123
EE973211	37	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	95
DY137128	53	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	111
CX060692	58	CCAGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	116
BM031252	33	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	91
BF076440	50	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	108
BI976230	48	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	106
BE808641	49	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	107
BE754888	33	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	91
BF775575	31	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	89
BY721079	92	GCTGGCCAGGTAGTGTGCGCTT-GGCTTACCAGCGCTTCGAGCCCGCGCCTATCTCCG	150
BE808590	29	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	87
CA392806	370	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	428
T27687	1	AGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	52
DY185707	43	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	101
DY080412	2	G	2
DY043824	43	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	101
DY077706	44	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	102
DY189365	157	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	215
DY079272	34	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	92
CD556603	412	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCTTCGAGCCCGCGCCTACCTCCG	470
BF829680	4	CCG	6
BU551882	23	GGCCAGGTAGTGTGCGCTT-GGCTTACCAGCGCTTCGAGCCCGCGCCTATCTCCG	78
DY082603	162	CCGGGCCAGGCGGCGGT-GGCTTCGGCCTACCAGCGCT	198

none in this region.

Query	117	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGGCCG	171
AV703309	113	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGGCCG	167
AV701492	41	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGGCCG	95
EL733651	111	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGGCCG	165

BM710229	60	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	114
BI819400	334	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	388
BP197959	131	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	185
BP197915	131	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	185
AW951884	52	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	106
BX926574	126	CAACAACCTACG-CGCCCCCTCGGGGGG-ACCTGAGC-AG-CCCAGAT-GGTGTGGGGCCT	180
BX674168	96	CAACAACCTACG-CGCCCCCTCGGGGGG-ACCTGAGC-AG-CCCAGAT-GGTGTGGGGCCT	150
BX667933	220	CAACAACCTACG-CGCCCCCTCGGGGGG-ACCTGAGC-AG-CCCAGAT-GGTGTGGGGCCT	274
AV705715	124	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	178
EE973211	96	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	150
DY137128	112	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGCGTCGGGCCT	166
CX060692	117	CAACAACCTACG-CGCCCCCTCGGGGGG-ACCTGAGC-AG-CCCAGAT-GGTGTGGGGCCT	171
BM031252	92	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	146
BF076440	109	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	163
BI976230	107	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	161
BE808641	108	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	162
BE754888	92	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGCGTCGGGCCT	146
BF775575	90	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	144
BY721079	151	CAACAACCTACG-CGCTCTCTCGTGGAG-ACCTGAGC-AA-CCCTGAT-GGCGTCGGGCCT	205
BE808590	88	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	142
CA392806	429	CAACAACCTACG-CGCCCCCTCGGGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	483
T27687	53	CAACAACCTACG-CGCCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	107
DY185707	102	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGCTGC-CCC-G-ACGGCGTCGGGCCT	156
DY080412	3	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	57
DY043824	102	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGCGTCGGGCCT	156
DY077706	103	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGCGTCGGGCCT	157
DY080460	1	GGGCCT	6
DY189365	216	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGCGTCGGGCCT	270
DY079272	93	CAACAACCTACG-CGCCCCCGAGGGGGG-ACCTGAGC-TG-CCCCGA-CGGTGTCTGGGCCT	146
CD556603	471	CAGCAACTA-GTCGTCCCGTCGGGGGGGACCTGTGC-AAACCC-GAACGGCGTCGGGCCT	526
BF829680	7	CTACTACTACG-CG-CCCCCTCGCGGGG-ACCTGTGC-AA-CCC-GAACGGCGTCGGGCGG	60
BU551882	79	CAACAACCTACG-CGCTCTCTCGTGGAG-ACCTGAGC-AA-CCCTGAT-GGCGTCGGGCCT	133
Query	172	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	228
BI457762	37	GGTGAAGTGTCCAGACGCACC	57
AV703309	168	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	224
AV701492	96	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	152
EL733651	166	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	222
EB523840	746	AGCTGCGCTGC-TGGCACA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	695
BM710229	115	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	171
BI819400	389	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	445
BP197959	186	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	242
BP197915	186	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	242
AW951884	107	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	163
BX926574	181	TGGA-AGCTGCGCTGCTTGGCCCA-GACCTTC-GCGACCGGTGAGGTGTCTGGACGCGCC	237
BX674168	151	TGGA-AGCTGCGCTGCTTGGCCCA-GACCTTC-GCGACCGGTGAGGTGTCTGGACGCGCC	207
BG394800	90	GGTGAAGTGTCCGGACGCACC	110
BX667933	275	TGGA-AGCTGCGCTGCTTGGCCCA-GACCTTC-GCGACCGGTGAGGTGTCTGGACGCGCC	331
DB489677	32	GGTGAAGTGTCCAGACGCACC	52
AV705715	179	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	235
EE973211	151	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	207
CK775040	722	GCACC	718
DY137128	167	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	223
CX060692	172	TGGA-AGCTGCGCTGCTTGGCCCA-GACCTTC-GCGACCGGTGAGGTGTCTGGACGCGCC	228
BE251193	70	GGTGAAGTGTCCGGACGCACC	90
BM031252	147	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	203
BF076440	164	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	220
BI976230	162	TGGA-AGCTGCGCTGCTTGGCTCA-AACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	218
BE808641	163	TGGA-AGCTGCGCTGCTTGGCTCA-TACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	219
BE754888	147	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	203
BF775575	145	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	201
BY721079	206	TGGA-AGCTGCGCTGCATGGCACAAGTCTTT--GCTACCGGTGAGGTGTCTGGGACGGGTT	262
BE808590	143	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	199
CA392806	484	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTGTCCGGACGCACC	540
T27687	108	TGGATAA-TNCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGAAGTNTCCGGACG-ACN	163
DY185707	157	TGGA-AGCTGC-CTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	212
DY080412	58	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGN-CC	113
DY043824	157	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	213
DY188095	1	GCTGCTTGGCTCA-GACCTTC-TGNCACCGGTGAGGTGTCTGGCCGCACC	48
DY077706	158	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	214
DY080460	7	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	63
DY189365	271	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	327
DY079272	147	TGGA-AGCTGCGCTGCTTGGCTCA-GACCTTC-GCCACCGGTGAGGTGTCTGGCCGCACC	203
BF829680	61	TGGA-AGCTGCGCTGCTTGGCGCA-GACCTTC-GCCACCGGTGA	101
BU551882	134	TGGA-AGCTGCGCTGCATGGC	153
Query	229	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	283
BI457762	58	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	112
BI913953	1	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	55
AV703309	225	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	279

AV701492	153	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	207
EL733651	223	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	277
EB523840	694	CTCATCGACATT-GGTTCA-GGCCCCA-CGTGTACCA-GCTGCTCAGC-G-CTGCAG-CC	642
BM710229	172	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	226
BI819400	446	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	500
BP197959	243	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	297
BP197915	243	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	297
AW951884	164	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	218
BX926574	238	CTCATCGACATT-GGTTCA-GGCCCCACCATATACCA-GCTGCTCAGC-GCCTGC-G-CC	291
BX674168	208	CTCATCGACATT-GGTTCA-GGCCCCACCATATACCA-GCTGCTCAGC-GCCTGC-G-CC	261
BG394800	111	TTCATCGACATTGGGTTCA-GGCCCCACCGTGTACCAGGCTGCTCAGT-GCCTGCAG-CC	167
BX667933	332	CTCATCGACATT-GGTTCA-GGCCCCACCATATACCA-GCTGCTCAGC-GCCTGC-G-CC	385
DB489677	53	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	107
AV705715	236	CTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	290
EE973211	208	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	261
BX667169	4	TGC-G-CC	9
CK775040	717	TTCATTGACATG-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTG-TGCC	663
DY137128	224	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	277
CX060692	229	CTCATCGACATT-GGTTCA-GGCCCCACCATATACCA-GCTGCTCAGC-GCCTGC-G-CC	282
BE251193	91	TTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGT-GCCTGCAG-CC	145
BM031252	204	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	257
BF076440	221	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	274
BI976230	219	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	272
BE808641	220	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	273
BE754888	204	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	257
BF775575	202	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	255
BY721079	263	CTCATTGATATT-GGCTCC-GGCCCCACCATATATACCA-GCTGCTCAGT-GCCTGT-G-CC	316
BE808590	200	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	253
CA392806	541	CTCATAGATATT-GGTTCA-GGCCCCACCGTGTACC	574
T27687	164	TTCATCGACATT-GGTTCA-GGCCCCACCGTGTACCA-GCTGCTCAGTTGCCTGCAG-CC	219
DY185707	213	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	266
DY080412	114	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	167
DY043824	214	CTCATCGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	267
DY188095	49	CTCATTGACATN-GGTTCA-CGACCCACTATATACCA-GCTGCTCAGC-GCCTG-TGCC	103
DY077706	215	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	268
DY080460	64	CTCATTGACATC-GGTTCA-GGACCCACTATATACCA-GCTGCTCAGC-GCCTGT-G-CC	117
DY083839	9	TACCA-GCTGCTCAGC-GCCTG-TGCC	33
DY189365	328	CTCATTGACAT	338
DY079272	204	CTCATTGACATC-GGTTCAAGGACCCAC	230
BU551882	166	TACC--GCTGCTCAGT-GCCTG-TGCC	189

Query	284	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	336
BI457762	113	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	165
BI913953	56	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	108
AV703309	280	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	332
AV701492	208	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	260
EL733651	278	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	330
EB523840	641	-ACTTTGAAGAC-ATT-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	589
BM710229	227	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	279
BI819400	501	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	553
BP197959	298	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	350
BP197915	298	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	350
AW951884	219	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	271
BX926574	292	CACTTTGAAGAC-ATC-ACCATGAC-TGATTTCTT-GG-AGGTGAA-CCGCCAGGAGCTG	345
BX674168	262	CACTTTGAAGAC-ATC-ACCATGAC-TGATTTCTT-GG-AGGTGAA-CCGCCAGGAGCTG	315
BG394800	168	-ACTTTGAGGACTATCAACCATGACTAGATTTTCCT-GGAAGGTCAA-CCGCCAGGAGCTG	224
BX667933	386	CACTTTGAAGAC-ATC-ACCATGAC-TGATTTCTT-GG-AGGTGAA-CCGCCAGGAGCTG	439
DB489677	108	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	160
AV705715	291	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	343
EE973211	262	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	315
BX667169	10	-AC-TTGAAGA--ATC-ACCATGAC-TGATTTCTT-GG-AGGTGAA-CCGCCAGGAGCTG	60
CK775040	662	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	610
DY137128	278	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	331
CX060692	283	CACTTTGAAGAC-ATC-ACCATGAC-TGATTTCTT-GG-AGGTGAA-CCGCCAGGAGCTG	336
BE251193	146	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGCCAGGAGCTG	198
BM031252	258	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	311
BF076440	275	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	328
BI976230	273	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	326
BE808641	274	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	327
BE754888	258	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	311
BF775575	256	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	309
BY721079	317	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTCAA-CCGTGAGGAGCTG	370
BE808590	254	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	307
T27687	220	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCTGG-AGGTCAAACCGCCAGGAGCTT	274
DY185707	267	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	320
DY080412	168	CACTTTGAAGAC-ATC-AC-ATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	220
DY043824	268	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	321
DY188095	104	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	156
DY077706	269	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	322
DY080460	118	CACTTTGAAGAC-ATC-ACCATGAC-AGATTTTCCT-GG-AGGTGAA-CCGCCAGGAGCTG	171

DY083839	34	-ACTTTGAGGAC-ATC-ACCATGAC-AGATTTCTT-GG-AGGTGAA-CCGCCAGGAGCTG	86
DV902079	3	C-ACCATGAC-TGA-TTGT-TG-GGGTGAA-CCGCCAGGAGCTG	41
BU551882	190	-ACTTTGAGGAC-ATC-ACCATGAC-AGACTTCTT-GG-AAGTCAA-CCGTCAAGGAGCTG	242
ES317490	355	AA-CCGCCAGGAGCTG	369
ES317140	355	AA-CCGCCAGGAGCTG	369
Query	337	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	388
BI457762	166	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	217
BI913953	109	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	160
AV703309	333	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	384
AV701492	261	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	312
EL733651	331	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	382
EB523840	588	GGGC-GCTGGCTG--AGG-GAGGAGCCAGGAG-CCTTCAACTGGAG--CATGTACA-GCC	537
BM710229	280	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	331
BI819400	554	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	606
BP197959	351	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	402
BP197915	351	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	402
AW951884	272	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	323
BX926574	346	GGAC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--TGCTTACA-GCC	397
BX674168	316	GGAC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--TGCTTACA-GCC	367
BG394800	225	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	276
BX667933	440	GGAC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--TGCTTACA-GCC	491
DB489677	161	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	212
AV705715	344	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	395
EE973211	316	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	367
BX667169	61	GGAC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--TGCTTACA-GCC	112
EE973212	641	GGCTGC---GAGGAGCCCTGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	597
CK775040	609	AGGT-TTTGGCTGC---GAAAGAGCTGGGG-CTTTGATTGGAG--GGTGTACA-GCC	558
DY137128	332	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	383
CX060692	337	GGAC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--TGCTTACA-GCC	388
BE251193	199	GGGC-GCTGGCTGC-A-G-GAGGAGCCGGGGG-CCTTCAACTGGAG--CATGTACA-GCC	250
BM031252	312	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	363
BF076440	329	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	380
BI976230	327	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	378
BE808641	328	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	379
BE754888	312	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	363
BF775575	310	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	361
BY721079	371	GGAC-TCTGGCTGCGA-G--AGGAGCCAGGAG-CCTTTGACTGGAG--TGCTGTATA-GTC	422
BE808590	308	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	359
T27687	275	GGG	277
DY185707	321	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACAAGCC	373
DY080412	221	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	272
DY043824	322	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	373
DY188095	157	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	208
DY077706	323	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	360
DY080460	172	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	223
DY083839	87	AGGC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--CGTGTACA-GCC	138
DV902079	42	GGAC-TCTGGCTGCGA-G-AAG-AGCCCGGGG-CCTTCGATTGGAG--TGCTTACA-GCC	93
BU551882	243	GGAC-TCTGGCTGC	255
DT397123	68	TGGCTGC-A-A-GACGAGCCTGGAG-CATTCGATTGGAGTCCA--TATA-TCA	113
ES317490	370	GAGAAG-TGGCTGA-A-G-AAGGAGCCGGGAG-CGTTTGACTGGA	409
ES317140	370	GAGAAG-TGGCTGA-A-G-AAGGAGCCGGGAG-CGTTTGACTGGA	409
Query	389	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	438
BI457762	218	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	267
BI913953	161	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	210
AV703309	385	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	434
AV701492	313	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	362
EL733651	383	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	432
EB523840	536	AGTATGCC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	487
BM710229	332	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	381
BI819400	607	AACATGCCCTGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	657
BP197959	403	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	452
BP197915	403	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	452
AW951884	324	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	373
BX926574	398	AGCACGTC-TGC-CTCATCGAGGGCAA-G-GGTGA-ATC-CTGCCA-GGAGAAG--G-AG	447
BX674168	368	AGCACGTC-TGC-CTCATCGAGGGCAA-G-GGTGA-ATC-CTGCCA-GGAGAAG--G-AG	417
BG394800	277	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	326
BX667933	492	AGCACGTC-TGC-CTCATCGAGGGCAA-G-GGTGA-ATC-CTGCCA-GGAGAAG--G-AG	541
DB489677	213	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	262
AV705715	396	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGTA-AGGACTGG	434
AV705715	537	GGA-ATGCCT-GCA-GGATAAG--G-AG	558
EE973211	368	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	417
BX667169	113	AGCACGTC-TGC-CTCATCGAGGGCAA-G-GGTGA-ATC-CTGCCA-GGAGAAG--G-AG	162
EE973212	596	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	547
CK775040	557	AGCATGTT-TGC-TTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	508
DY137128	384	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	433
CX060692	389	AGCACGTC-TGC-CTCATCGAGGGCAA-G-GGTGA-ATC-CTGCCA-GGAGAAG--G-AG	438
BE251193	251	AACATGCC-TGC-CTCATTTAGGGGCAA-G-GGGGA-ATG-CTGGCA-GGATAAG--G-AG	300
BM031252	364	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	413

BF076440	381	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	430
BI976230	379	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	428
BE808641	380	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	429
BE754888	364	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	413
BF775575	362	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	411
BY721079	423	AGCATGCC-TGC-CTCATCGAGGGCAA-G-GGTGA-GTC-CTGGCA-GGAGAAA--G-AA	472
BE808590	360	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	409
DY185707	374	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	405
DY080412	273	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	322
DY043824	374	AGCATGTC-TGC-CT	386
DY188095	209	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	258
DY080460	224	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	273
DY083839	139	AGCATGTC-TGC-CTCATCGAGGGCAA-G-GGGGA-ATC-CTGGCA-GGAGAAG--G-AG	188
DV902079	94	AGCACGTC-TGG-CTCATCGAGGGCAA-G-GGTGA-ATC-CTGGCA-GGAGAAG--G-AG	143
DT397123	114	AACATGTC-AGCAAGC-TTGAGGG-AA-GAGGGGACA-G-CTGGCA-GGAGAAGCAGAAG	166
CV359995	311	GGCAGGGATAAG--G-AG	297

462

Query	439	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	492
BI457762	268	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	321
BI913953	211	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	264
AV703309	435	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	488
AV701492	363	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	416
EL733651	433	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	486
EB523840	486	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	433
BM710229	382	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	435
BI819400	658	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GGTCTTGGCCAT-CGACGTGCACCAGCCG	713
BP197959	453	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	506
BP197915	453	CGCCAGCTGC-GAGCCAGGGTGNN-ACG-GGTCTT-GCCCAT-CGACGTGCACCAGCCC	507
AW951884	374	TGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	427
BX926574	448	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GA-TCCT-GCCCAT-CGACGTGCACCAGCCC	501
BX674168	418	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GA-TCCT-GCCCAT-CGACGTGCACCAGCCC	471
BG394800	327	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	380
AV703457	4	CG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	33
BX667933	542	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GA-TCCT-GCCCAT-CGACGTGCACCAGCCC	595
DB489677	263	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	316
AV705715	559	CGCCAGCTGC-GAGCCCGGGGGAA-ACG-GG-TTCT-GCCCAT-TGCCG-GCACCACCC	611
EE973211	418	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	471
BX667169	163	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GA-TCCT-GCCCAT-CGACGTGCACCAGCCC	216
EE973212	546	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	493
CK775040	507	TGCCAGTTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	454
DY137128	434	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	487
CX060692	439	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GA-TCCT-GCCCAT-CGACGTGCACCAGCCC	492
BE251193	301	CGCCAGCTGC-GAGCCAGGGTGAA-ACG-GG-TCCT-GCCCAT-CGACGTGCACCAGCCC	354
BM031252	414	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	467
BF076440	431	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	484
BI976230	429	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	482
BE808641	430	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	483
BE754888	414	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	467
BF775575	412	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	465
BY721079	473	CGCCAGCTTC-GAGCGAGGGTGAA-GCG-AG-TCCT-GCCTAT-CGATGTGCACAAGCCC	526
BE808590	410	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CTATGTGCACCGGCC	463
DY080412	323	TGCCAGCTGC-GAACCAGGGTGAA-GA-GA-TCCT-GCCCAT-CTATGTGCACCGGCC	376
BE106746	504	CAGCTCC-GAGCGAGGGTGAA-GCG-AG-TCTT-GCCCAT-TGATGTGCACAAGCCC	454
DY188095	259	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGCACCGGCC	312
DY080460	274	TGCCAGCTGC-TAGCCAGGGTGAA-A-GAGGATCCT-GCC	309
DY083839	189	TGCCAGCTGC-GAGCCAGGGTGAA-GA-GA-TCCT-GCCCAT-CGATGTGC	234
DV902079	144	CGCCAGCTGC-GAGCCAGGGTGAA-GCG-GA-TCCT-GGCCAT-CGACGTGCACCAGCCC	197
DT397123	167	CG-CATCCGG-GAG-C-GGGTAAAGAC--GG-TGCT-GCCGGT-GGATGTTTCATCAGCCC	217
EG819500	293	C	293
DA184445	285	CCAGCCC	279
CV359995	296	CGCCAGCTGCAGAG	283

Query	493	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	536
BI457762	322	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	365
BI913953	265	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	308
AV703309	489	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	532
AV701492	417	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	460
EL733651	487	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	530
EB523840	432	CAGCCCCCT-G-GG-TAC-TGG-GA-G-CCCAG-C-G-CCC-CTGCC--TG-CC-GAC-AC	389
BM710229	436	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	479
BI819400	714	CAGGCCCT-G-GG-TGC-TGG-GA-G-CC-AG-C-T-CCC-CTGCC--TG-GT-GAC-GC	756
BP197959	507	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	550
BP197915	508	CAGCCCCCT-G-GG-TGC-TGGNGA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	552
AW951884	428	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAA-C-T-CCC-CTGCC--TG-CT-GAC-CC	471
BX926574	502	CAGCCCCCT-G-GG-CAC-CGG-GA-G-CTTGG-C-G-CCC-CTGCC--TG-CC-GAT-GC	545
BX674168	472	CAGCCCCCT-G-GG-CAC-CGG-GA-G-CTTGG-C-G-CCC-CTGCC--TG-CC-GAT-GC	515
BG394800	381	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	424
AV703457	34	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	77
BX667933	596	CAGCCCCCT-G-GG-CAC-CGG-GA-G-CTTGG-C-G-CCC-CTGCC--TG-CC-GAT-GC	639
DB489677	317	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	360

AV705715	612	AAGCCC-T-G-G--TGC-TGG--A-G-CCCAG-T-T-TCC--TGGC--TG-CT-GAC-GC	651
BX280348	446	TGCC--TG-CT-GAC-GC	434
EE973211	472	CAGCCCCCT-G-GG-TGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	515
BX667169	217	CAGCCCCCT-G-GG-CAC-CGG-GA-G-CTTGG-C-G-CCC-CTGCC--TG-CC-GAT-GC	260
EE973212	492	CAGCCCCCT-G-GG-TGC-T-G-GAGG-CCTGG-C-A-CCC-CTGCC--TG-CC-GAC-GC	449
CK775040	453	CAGCCCCCT-G-GG-TGC-T-G-GAGG-CCTGG-C-A-CCC-CTGCC--TG-CC-GAC-GT	410
DY137128	488	CAGCCCCCT-G-GG-TGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	531
CX060692	493	CAGCCCCCT-G-GG-CAC-CGG-GA-G-CTTGG-C-G-CCC-CTGCC--TG-CC-GAT-GC	536
BE251193	355	CAGCCCCCT-G-GG-TGC-TGG-GA-G-CCCAG-C-T-CCC-CTGCC--TG-CT-GAC-GC	398
AI880325	369	CCT-G-GG-TGC-TGG-GA-GCCCCAG-CTT-CCC-CTGCC--T--CT-GAC-GC	330
BM031252	468	CAGCCCCCT-G-GG-TGC-TGG-NA-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	512
BF076440	485	CAGCCCCCT-G-GG-TGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	528
BI976230	483	CAGCCCCCT-G-GG-TGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	526
BE808641	484	CAGCCCCCT-G-GGTGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	528
BE754888	468	CAGCCCCCT-G-GG-TGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-C	505
BF775575	466	CAGCCCCCT-G-GG	476
BY721079	527	CAGCCCCCT-G-GG-AAC-TCC-CA-G-TCTGG---T-CCCTCTGCC--TG-CC-GAC-GC	570
BE808590	464	CAG	466
DY080412	377	CA	378
BE106746	453	CAGCCCCCT-G-GG-AGCTTCG-G--G-CCTGG-C-A-CCC-CTGCC--TG-CT-GAC-GC	410
DY188095	313	-AGCCCCCT-G-GG-TGC-TGG--A-G-GCCTGGC-A-CCC-CTGCC--TG-CC-GAC-GC	355
DV902079	198	CAGCCCCCT-G-GG-CAC-CGG-GA-G-CTTGG-C-G-CCC-CTGCC--TGCC--GAT-GC	241
DT397123	218	AATCCCCCTAG-GG--G---AG-GA-G-ATAAG-CAG-CGG-CT-CC---G--TGGAT-GC	258
CX260010	537	CCAG-C-TCCCCACTGCCGGCG-CC-GACTG-	510
EG819500	294	CAGCCCCCT-G-GG-TGC-TGG-GA-G-C	314
DA184445	278	CAGCCCCCT-GTGG--GC-TGA-GA-G-CCCA	255

Query	537	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	588
BI457762	366	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	417
BI913953	309	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	360
AV703309	533	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	584
AV701492	461	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	512
EL733651	531	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	582
EB523840	388	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TC-	337
BM710229	480	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	531
BI819400	757	C-CTGGTCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AG-T-TT-	808
BP197959	551	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGA	582
BP197915	553	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TG	581
AW951884	472	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGGGAGCCCAGAACTTGCC-AGCT-TT-	523
BX926574	546	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	597
BX674168	516	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	567
BG394800	425	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	476
AV703457	78	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	129
BX667933	640	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	691
DB489677	361	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	412
AV705715	652	C--TGG--CT-CTGGCTT-TGCT	668
BX280348	433	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	382
EE973211	516	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	567
BX667169	261	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	312
EE973212	448	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	397
AV725746	1	CCCAGATCTTGCC-AGCT-TT-	19
CK775040	409	T-TTGG-TTT-TTGCCTTTTGCCTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-TC-	358
DY137128	532	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGC	580
CX060692	537	C-CTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGTCCAGACCTGGCC-AGCT-T	587
BE251193	399	C-CTGG-TCT-CTGCCTTCTGCTTGG	420
AI880325	329	CNC-GG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTGCC-AGCT-TT-	278
BM031252	513	T-CTGG-TCT-CTGCCTTCTGCT	531
BF076440	529	T-CTGG-TCT-CTGCCTTCTGCT	547
BI976230	527	T-CTGG-TCT-CTGCCTTCTGCTTGG-A	550
BE808641	529	T-CTGG-TCT-CTGCCTTCTGCT	547
BY721079	571	C-TTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCAGATCTTACT-AGCT-TC-	622
BE106746	409	C-TTGG-TCT-CTGCCTTCTGCTTGG-AGGC-TGTGAGCCCGGATC-TCCCAAGCT-TC-	358
DY188095	356	C-CTGG	360
DV902079	242	C-CTGG-TCT-CTGCCTTCTG	259
DT397123	259	G-TTGG-TAT-CTACCTTCTGCTTGG-AGGCCTGC-AGCCCAAA-CTTGG--AGATGTTT	310
DT397124	608	TGG-TAT-CTACCTTCTGCTTGG-AGGCCTGC-AGCCCAAA-CTTGG--AGATGTTT	559
CX260010	509	C-CTGG-TGTCTG-CTTCTGCTTGGAAAGC--GTCAGTCTGACCTGGCC--TCC-TT-	459

Query	589	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGGGGGCA-CCT	638
BI457762	418	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGGGGGCA-CCT	467
BI913953	361	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGGGGGCA-CCT	410
AV703309	585	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CTTG-T-GAGGCCCTGGGGGGCA-CCT	634
AV701492	513	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGGGGGCA-CCT	562
EL733651	583	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGNGGGCA-CCT	632
EB523840	336	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGAGGGCA-CCT	287
BM710229	532	CA-GCGGGCCCCCT-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGGGGGCA-CCT	582
BI819400	809	CA-GCGGGGCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCCTGGGGGGCA-CCT	853
AW951884	524	CA-GCGGGCCCCCT-GG-ACCACATC-ACCAC-G-CTTG-T-GAGGCCCTGGGGGGCAACCT	576
BX926574	598	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-A-CT-GCT-GAGGTCTGGAGGGCA-CCT	647
BX674168	568	CA-GCGGGCCC-T-GG-ACCACATC-ACCAC-A-CT-GCT-GAGGTCTGGAGGGCA-CCT	617

BG394800	477	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCTGGGGGGCA-CCT	526
AV703457	130	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCTGGGGGGCA-CCT	179
BX667933	692	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-A-CT-GCT-GAGGTCTGGAGGGCA-CCT	741
DB489677	413	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCTGGGGGGCA-CC	461
BX280348	381	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCTGGGGGGCA-CCT	332
EE973211	568	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-A-CT-G	597
BX667169	313	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-A-CT-GCT-GAGGTCTGGAGGGCA-CCT	362
EE973212	396	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-A-CT-GCT-GAGGCCTGGGGGGCA-CCT	347
AV725746	20	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-G-CT-GCT-GAGGCCTGGGGGGCA-CCT	69
CK775040	357	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-A-CT-GTT-GAGGCCTGGGGGGCA-CCT	308
AI880325	277	CA-GCGGGCCCC-T-GG-ACCACATC-ACCAC-G-CT-G-T-GAGGCCTGGGGGGCA-CCT	229
BM664183	339	GAGGCCTGGGGGGCA-CCT	322
BY721079	623	CA-GCGG-CCT-T-TGCATCACATC-ACCAC-A-CT-GCT-GAGGCCCGGGGNTCA-TCT	672
N63192	308	CT	307
BE106746	357	CG-GCAGGCTT-T-GT-ATCATATC-ACGAC-G-CT-GCT-GAGGCCCGGGGGTCA-TCT	308
BM658761	361	GGGCCC-T-GG-ACCACATC-ACCAC-A-CT-GCT-GAGGTCTGGAGGGCA-CCT	316
BE752632	1	A-CCT	4
BE752631	1	A-CCT	4
BE110952	339	ATC-ACGAC-G-TT-GTT-GAGGCCCGGGGGTCA-TCT	308
DT397123	311	CA-TAGGGCCCC-TTGGTA--ACATC-ACCAA-A-CT-GTT-GAAGCCCGGGGGCCA-CTT	360
DT397124	558	CA-TAGGGCCCC-TTGGTA--ACATC-ACCAA-A-CT-GTT-GAAGCCCGGGGGCCA-CTT	509
CX260010	458	CACCCGGGCCCC-T-GG-GCCACATC-A-GGG-GCCT-TCT-CCGGCCCGGGGGCCA-CCT	408

Query	639	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	691
BI457762	468	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	520
BI913953	411	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	463
AV703309	635	N-C-TNC-TCATC-GGG-GCCNT-G-AGGAGTCGTGGTACCTGGCTGGGAAGGCAAG-C	686
AV701492	563	N-C-TNC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGNGAGGCCAGGC	615
EL733651	633	C	633
EB523840	286	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCATGGTACCTGGCTGGGGAGGCCAGGC	234
BM710229	583	C-C-TCC-TCATC-G	593
AW951884	577	T-C-TCT-T-ATTTGGG-GCCC-TTGGAGGAATCCTGGTACC	612
BX926574	648	G-C-TCC-TCATC-GGG-GCCT-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	700
BX674168	618	G-C-TCC-TCATC-GGG-GCCT-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	670
BG394800	527	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	579
AV703457	180	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	232
BX667933	742	G-C-TCC-TCATC-GGG-GCCT-T-GGAGGAGTCGTGGTACCT	777
BX280348	331	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	279
BX667169	363	G-C-TCC-TCATC-GGG-GCCT-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	415
EE973212	346	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCATGGTACCTGGCTGGGGAGGCCAGGC	294
AV725746	70	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	122
CK775040	307	C-C-TCT-TCATC-GGG-GCCC-T-GGAGGAGTCATGGTACCTGGTTGGGGAGGCCAGGC	255
AI880325	228	C-CNCCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	175
BM664183	321	C-C-TCC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	269
BY721079	673	CNC-TCT--TCAT	681
N63192	306	C-C-TCCTTCATC-GGGAGCCN-T-GGAGGAGTCGTGGTACNTGGCTGGGGAGGCCAGGC	252
BE106746	307	C-C-TTC-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTTGCTGGGGAGGCCAGGC	255
BM658761	315	G-C-TCC-TCATC-GGG-GCCT-T-GGAGGAGTCGTGGTACCTGGCTGGGGAGGCCAGGC	263
BE752632	5	C-C-TCC-TCATC-GGA-GCCC-T-GGAGGAGTCATGGTACCTGGCTGGGGAGGCCAGGC	57
BE752631	5	C-C-TCC-TCATG-GGG-GGCC-T-GGAGGAGTCATGGTACCTGGCTGGGGAGGCCATGC	57
BE110952	307	C-C-TTT-TCATC-GGG-GCCC-T-GGAGGAGTCGTGGTACCTTGCTGGGGAGGCCAGGC	255
DT397123	361	G-C-TCT-TCATT-GGT-GCCT-T-GGAGGAGTCGTATTATTGGCCGGAGAGGCCAAGC	413
DT397124	508	G-C-TCT-TCATT-GGT-GCCT-T-GGAGGAGTCGTATTATTGGCCGGAGAGGCCAAGC	456
CX260010	407	G-C-TCC-TCATC-GGG-GCCC-T-GG	388

Query	692	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	742
BI457762	521	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	571
BI913953	464	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	514
AV703309	687	-TGA-CGGTGGTGC-ANTGG-C-TGAGGAGGAG--T-AGG-AG-GCCT-TG-TGC-GTA-	732
AV701492	616	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGG	660
EB523840	233	-TGA-TGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	183
BX926574	701	-TGG-CAGTGGTGCCCTGTGT-G-TGAGGAGGAG-GTGAGGGAG-GCTC-TGGCAC-GTA-	751
BX674168	671	-TGG-CAATGGTGCCCTGTGT-G-TGAGGAGGAG-GTGAGGGAG-GCTC-TGGCAC-GTA-	721
BG394800	580	-TGA-CGGTGGTGCC-GTGT-C-TGAGGAGGAG	607
AV703457	233	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	283
BX280348	278	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	228
BX667169	416	-TGG-CAGTGGTGCCCTGTGT-G-TGAGGAGGAG-GTGAGGGAG-GCTC-TGGCAC-GTA-	466
EE973212	293	-TGG-CGGTGGTGCCCGTG--CGCGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GGA-	243
AV725746	123	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTG-	173
CK775040	254	-TGG-CGGTGGTGCCCGTG--CGCGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GGA-	204
AI880325	174	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	124
BM664183	268	-TGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	218
N63192	251	TTGA-CGGTGGTGCCAGTGT-C-TGAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GTA-	200
BE106746	254	-T-ATCTGTGGTTCCAGTGT-C-AGAGGAGGAG-GTGAGGGAG-GCCC-TGGT-CTGTA-	204
BM658761	262	-TGG-CAGTGGTGCCCTGTGT-G-TGAGGAGGAG-GTGAGGGAG-GCTC-TGGCAC-GTA-	212
BE752632	58	-TGG-CGGTGGTGCCCGTGCGC--GAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GGA-	108
BE752631	58	-TGG-CGGTGGTGCCCGTGCGC--GAGGAGGAG-GTGAGGGAG-GCCC-TGGTGC-GGA-	108
BE110952	254	-T-ATCTGTGGTTCCAGTGT-C-AGAGGAGGAG-GTGAGGGA--GCCCTTGGT-CTGTA-	204
BF408734	250	GTGGTTCCAGTGT-C-AGAGGAGGAG-GTGAGGGAG-GCCC-TGGT-CTGTA-	205
DT397123	414	-TGA-ATGTAGTTCCTGTC-A-AGAGGAG-ATCGT-ACGAAACGCGC-TG-TCC-G-AC	463

DT397124 455 -TGA-ATGTAGTTCCTCCGTCA-C-AGAGGAG-ATCGT-ACGAAACGCGC-TG-TCC-G-AC 406

Query	743	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	795
BI457762	572	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	624
BI913953	515	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	567
AV703309	733	ATG--CTACAAG-TCCCG-ACACTCC-G-ACTTTT--T-ATGCCTGCA-AC-CTT-AA--	778
EB523840	182	GTG-GCTACGAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	130
BX926574	752	GCG-GCTACGAGGTGCGGGAC-TTGC-GCACCTAT-GTCATGCCGGGCCAC-CTTNC-G-	804
BX674168	722	GCG-GCTACGAGGTGCGGGAA-CTGC-GCACCTAT-GTCATGCCGGGCCAG-CTT-CGG-	774
AV703457	284	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	336
BX280348	227	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	175
BX667169	467	GCG-GCTACGAGGTGCGGGAC-TTGC-GCACCTAT-GTCATGCCGGGCCAC-CTT-CGG-	519
EE973212	242	GCG-GCTACGAGGTGCGGGAT-CTGC-GCACCTAC-ACCATGCCTGCCCAC-CTT-CAG-	190
AV725746	174	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	226
CK775040	203	GCG-GTTACGAGGTGCGGGAT-TTGC-GCACCTAC-CCCATGCCTGCCCCC-CTT-CAG-	151
AI880325	123	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	71
BM664183	217	GTG-GCTACAAGGTCCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	165
N63192	199	GTG-GCTACAA-----GG----TCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CAG-	156
BE106746	203	GTG-GTTATGAGGTCCGAGAC-CTTC-GCACCTAC-ATCATGCCTGCCCAC-CTC-C-GC	151
BM658761	211	GCG-GCTACGAGGTGCGGGAC-CTCC-GCACCTAT-ATCATGCCTGCCCAC-CTT-CGG-	159
BE752632	109	GCA-GCTATGAGGTGCGGGAT-CTGC-GCACCTAC-ACCATGCCTGCCCAC-CTT-CAG-	161
BE752631	109	GCA-GCTATGAGGTGCGGGAT-CTGC-GCACCTAC-ACCATGCCTGCCCAC-CTT-CAG-	161
DR980845	10	CCAC-C-T-CAG-	18
BE110952	203	GTG-GTTATGAGGTCCGAGAC-CTTC-GCACCTAC-ATCATGCCTGCCCAC-CTC-C-GC	151
DB559237	1	TGCCC-C-CTTCCA--	12
BF408734	204	GTG-GTTATGAGGTCCGAGAC-CTTC-GCACATAC-ATCATGCTTGCCCAC-CTC-C-GC	152
DT397123	464	GCCAGCTACAAGATCAAGGAG-TTTAAG-ACCTAC-ATCATGCCC-CCCACACTA-AAG-	517
DT397124	405	GCCAGCTACAAGATCAAGGAG-TTTAAG-ACCTAC-ATCATGCCC-CCCACACTA-AAG-	352
CN000669	149	C-CTT-CAG-	143
CJ705520	211	CAAGGTCCGGGAC-CTCA-GCACC-ATCATCATG	241
CJ600022	423	CAAGGTCCGGGAC-CTCA-GCACC-ATCATCATG	393

Query	796	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	844
BI457762	625	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	673
BI913953	568	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	616
AV703309	779	A-CAG-CGTA-ATG-ATG-CAA	795
EB523840	129	A-CAGGTGTAGATG-ACGT-CAA-GGGCA-TCTT-CTTCGCCTGGGCTCAGAA---G--G	81
BX926574	805	A-CAGGCGTTGACG-ATGTNCA--GGGCA-TCTTTCTT-GCCTGGG	844
BX674168	775	A-CAG-CGTTGACA-ATGT-CA--GGGA--TCT--CTTTGCCGGGGC-CAGAA---G	817
AV703457	337	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	385
BX280348	174	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	126
BX667169	520	A-CAGGCGTGGACG-ATGT-CAA-GGGCA-TCTT-CTTCGCCTGGGCCCAGAA---GAAG	570
EE973212	189	A-CAGGTGTAGACG-ATGT-CAA-GGGCA-TCTT-CTTCACCCGGGCCCAGAA---GAAG	139
AV725746	227	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	275
CK775040	150	A-CAGGTGTAGACG-ATGT-CAA-GGGCT-TTTT-TTTCACCCGGGCCCCAAAAAAG--G	99
AI880325	70	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	22
BM664183	164	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	116
N63192	155	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	107
BE106746	150	A-CGGGTGTGGATG-ACGT-CAA-GGGTA-TCTT-CTTTGCCTGGGCCCAGAA---G	103
BM658761	158	A-CAGGCGTGGACG-ATGT-CAA-GGGCA-TCTT-CTTTGCCTGGGCCCAGAA---GAAG	108
BE752632	162	A-CAGGTGTAGACG-ATGT-CAA-GGGCA-TCTT-CTTCACCTGGGCCCAGAA---GAAG	212
BE752631	162	A-CAGGTGTAGACG-ATGT-CAA-GGGCA-TCTT-CTTCACCTGGGCCCAGAA---GAAG	212
DR980845	19	A-CAGGCGTAGATG-ATGT-CAA-GGGCG-TCTT-CTTCGCCTGGGCTCAGAA---G--G	67
BE110952	150	A-CGGGTGTGGATG-ACGT-CAA-GGGTA-TCTT-CTTTGCTTGGGCCCAGAA---G	103
DB559237	13	ACCA-GCCTTGATGAAT-T-TAA-GGGCGTTTTT-TTTC-CCTGGGGTCAAAA---G--G	61
BF408734	151	A-CGGGTGTGGATG-ACGT-CAA-GGGTA-TCTT-CTTTGCCTGGGCCCAGAA---G	104
DT397123	518	GTCGGG-GTAGATG-ATGT-CAATGGG-G-TGTT-TTTTGCCTGGGCCCAGAA	564
DT397124	351	GTCGGG-GTAGATG-ATGT-CAATGGG-G-TGTT-TTTTGCCTGGGCCCAGAA	305
CN000669	142	A-CAGGTGTAGACG-ACGT-CAA-GGGCA-TCTT-CTTCGCCTGGGCCCAGAA---G	95

Query	845	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	893
BI457762	674	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCC-ACC-AC-CTGG	720
BI913953	617	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	665
EB523840	80	TTGGAC-TGTGAGGGGCCA-GCGT--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	28
AV703457	386	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	434
BX280348	125	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	77
BX667169	571	GTGGGGGTGTGAGG	584
EE973212	138	TTGGGGGTGTGAGGC-CCCCG--TGCACGCAG-G-GCCAA-TGGCCCTCACCCTGC-CTAG	86
AV725746	276	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	324
CK775040	98	TGGGGG-TGTGAGGC-CCCCG--TGCACGCAG-G-GCCAA-TGGCCCTCACCCTGC-CTAG	47
AI880325	21	TTGGGC-TGTGAGGG-CT--G--T--AC-C	1
BM664183	115	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	67
N63192	106	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	58
BM658761	107	GTGGGGGTGTGAGGC-CCCAG--C--ACACCCAGTGCCG-GCATCCCTCACCACGCCG-	55
BE752632	213	GTGGGGGTGTGAGGC-CCCCG--TGCACGCAG-G-GCCAA-TGGCCCTCACCCTGC-CTAG	265
BE752631	213	TGGGGG-TGTGAGGC-CCCCG--TGCACGCAG-G-GCCAA-TGGCCCTCACCCTGC-CTAG	264
DR980845	68	TTGGGC-TGTGAGGG-CT--G--T--AC-CTG-GTGCCCTGTGGCCCCCACCAC-CTGG	116
DB559237	62	TTGGGC-TGTTAGGG-CT--T--T--AC-CTG-GTTCCCTTTGGCCCCCACCAC-CTGG	110

Query 894 ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC 936

BI457762	721	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AAATAAAGA-AA-TTATACC	764
BI913953	666	ATT-CCCTGTTCTTTGAAGTGTAC-CT-AA-TACAGA-AA	701
EB523840	27	ATT-CCCTTTTCTT-GAATTGGCAC-CT-AA	1
AV703457	435	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	477
BX280348	76	ATTTCCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	33
EE973212	85	ACT-CCCTGTTGTCTGAGGTGGC-CTCT-AA-TAAAGA-AA-TAA	47
AV725746	325	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	367
CK775040	46	ACT-CCCTGTTGTTTGAAGTGGC-C-TTTAA-TAAAAA-AA-TAA	8
BM664183	66	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	24
N63192	57	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	15
BM658761	54	AGT-CCCTGTTATCTGAGGTGACGT-CT-AA-TAAAGA-AA-TAA	16
BE752632	266	ACT-CCCTGTTGTCTGAGGTGGC-CTCT-AA-TAAAGA-AA-TAA	304
BE752631	265	ACT-CCCTGTTGTCTGAGGTGGC-CTCT-AA-TAAAGA-AA-TAA	303
DR980845	117	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	159
DB559237	111	ATT-CCCTGTTCTTTGAAGTGGCAC-CT-AA-TAAAGA-AA-TAATACC	153
BM874128	498	TTTGAAATGGCAC-CT-AA-TAAAGATAAGTAATA	467

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions

Posted date: Jun 7, 2007 6:28 PM

Number of letters in database: -1,965,808,602

Number of sequences in database: 43,364,352

Lambda	K	H
1.33	0.621	1.12

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 43364352

Number of Hits to DB: 5658775

Number of extensions: 1494

Number of successful extensions: 1482

Number of sequences better than 10: 10

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 1474

Number of HSP's successfully gapped: 11

Length of query: 936

Length of database: 23803995170

Length adjustment: 32

Effective length of query: 904

Effective length of database: 22416335906

Effective search space: 20264367659024

Effective search space used: 20264367659024

A: 0

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 12 (23.3 bits)

S2: 22 (41.7 bits)